CLAIMS

1. A method for immobilising a protein on a microporous material, said microporous material is selected from the group consisting of zeolite or similar solid surfaces whereby loss of activity of said protein is less than 10% of the initial activity prior to immobilising, the method comprising the steps of:

(i) selecting a polypeptide tag capable of binding to the surface,

(ii) immobilise said protein by the steps of:

(a) attaching said polypeptide tag to the protein, and

(b) binding said polypeptide tag to the solid surface

where step (a) and (b) is performed simultaneously or sequentially and when performed sequentially, the order of step (a) and (b) is random, subject to the limitation that the polypeptide tag does not consist only of histidine residues.

2. A method according to claim 1 wherein the binding in step (i) is a specifically binding of the polypeptide tag to the surface.

3. A method according to claim 1 or 2 wherein the polypeptide tag comprises at least two lysine residues.

4. A method according to any of claims 1-3 wherein the polypeptide tag comprises at the most 21-500 of amino acid residues.

5. A method according to any of claims 1-4 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 1.

6. A method according to any of claims 1-4 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 2.

7. A method according to any of claims 1-6 wherein the binding in step (i) is enhanced by repeating said polypeptide tag at least 2, 3, 4, 7, 10, 50, 100 times.

8. A method according to any of claims 1-7 wherein the avidity of the polypeptide tag for the surface is enhanced by repeating said polypeptide tag at least 2, 3, 4, 7, 10, 50, 100 times.

9. A method according to claim 7 or 8 wherein the amino acid sequence identity between the repeating polypeptide sequences is at least 30-100%.

10. A method according to any of claims 1-9 wherein the protein is a protein expressed on the surface of a cell.

11. A method according to any of claims 1-10 wherein said attachment of the polypeptide tag to the protein provides a fusion protein.

12. A method according to claim 11 wherein said fusion protein is recombinantly provided.

13. A method according to any of claims 1-12 wherein the polypeptide tag is attached to the protein by chemical treatment.

14. A method according to any of claims 1-13 wherein the surface comprises at least one aluminum moiety, at least one silicate moiety and/or at least one phosphate moiety.

15. A method according to any of claims 1-14 wherein the similar solid surface is selected from the group consisting of meso- and microporous materials including hydrotalcite, clay, aluminosilicate, oxide powders, activated carbon, mica, glass, clinoptolite, gismondine zeolite, alluminate and quartz.

16. A method according to claim 15 wherein the zeolite is either naturally occurring or synthetically produced.

17. A method according to any of claims 15 or 16 wherein the meso- and microporous material is selected from the group of zeolites consisting of AFI, EMT, FAU and MFI.

18. A method according to any of claims 15-17 wherein the zeolite has a pore size in the range of 1-50 Å, such as 1-40 Å, e.g. 1-30 Å, such as 1-20 Å, e.g. 1-15 Å, such as 2-10 Å, e.g. 3-8 Å, such as 5-8 Å, e.g. 6-8 Å.

19. A method according to any of claims 1-18 wherein the protein is selected from the group consisting of an antibody, an antigen, a receptor, a biotin, an avidin, a hormone, a lectin, a sugar, an enzyme and a protease.

20. A method according to any of claims 1-19 wherein the polypeptide tag is bound directly to the solid surface.

21. A polypeptide tag that is capable of controlling the orientation of proteins immobilised on a microporous material, said microporous material is selected from the group consisting of zeolite or similar solid surfaces.

22. A polypeptide tag according to claim 21 wherein the polypeptide tag comprises at least two lysine residues.

23. A polypeptide tag according to claim 21 or 22 wherein the polypeptide tag comprises at the most 21-500 amino acid residues.

24. A polypeptide tag according to any of claims 21-23 wherein the polypeptide tag is provided on at least one subunit of a protein.

25. A polypeptide tag according to any of claims 21-24 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 1.

26. A polypeptide tag according to any of claims 21-24 wherein said polypeptide tag has at least 30-100% amino acid sequence identity to SEQ ID NO 2.

27. A method for isolating an analyte from a liquid sample, said method comprises the steps of:

(i) selecting a protein immobilised according to the method of any of claims 1-20, said protein is capable of specifically binding to the analyte,

(ii) contacting said immobilised protein with the liquid sample,

(iii) permitting said immobilised protein to react with the analyte to obtain a complex of the immobilised protein and the analyte,

(iv) optionally washing said complex, and

(v) eluting the analyte from said complex.

28. A method according to claim 27 wherein the liquid sample is selected from the group consisting of a fermentation medium, wastewater, blood, milk and urine, diary products and/or chemical reaction.

29. A method according to any of claims 27-28 wherein the immobilised protein is reused.

30. Use of a protein immobilised according to the method of any of claims 1-20 as chromatography column material for the purification of an analyte.

31. Use of a protein immobilised according to the method of any of claims 1-20 for the hydrolysis of a molecule.

32. A cell comprising a surface molecule comprising the polypeptide tag according to any of claims 21-26.

33. A material having at least one surface onto which a polypeptide tag has been bound, said polypeptide tag has at least 30-100% identity to SEQ ID NO. 1 or SEQ ID NO. 2.

34. A material according to claim 33 wherein the surface is selected from the group consisting of meso- and microporous materials including zeolite, hydrotalcite, clay, aluminosilicate, oxide powders, activated carbon, mica, glass, clinoptolite, gismondine zeolite, alluminate and quartz.

35. A fusion protein having a polypeptide tag bound, said polypeptide tag has at least 30-100% identity to SEQ ID NO. 1 or SEQ ID NO. 2.